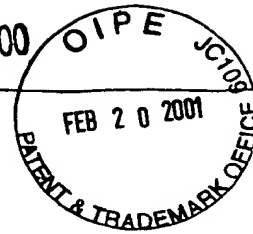


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SEQUENCE LISTING

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a1 <110> BOYLE, WILLIAM
LACEY, DAVID
CALZONE, FRANK
CHANG, MING-SHI
SENALDI, GIORGIO

<120> COMBINATION THERAPY FOR CONDITIONS LEADING TO BONE LOSS

<130> A-378CIP5

<140> US 09/613,591

<141> 2000-07-10

<150> US 09/457,647

<151> 1999-12-09

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<210> 31
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<400> 41
cctctgtcga ctattataag cagcttattt tcacggattg 40

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aaaaggaagc gtacgggtgc gatttgtaag aaaaagagaa aaccaattta gcaacaaact 540
aaataataaa cgatataaat aaaaagctat taatagttga tctcttcctt gttaattacc 600
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aagttttatat aagggttaatt agccacttac taacctcaat cttattagat gatatcctag 840
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tatgttaaca aattgtattc atggacatcc tagcatgtcc aaatgcgttc ttttaccaaa 1260
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aaccgacgac ggtggcgact cgttattgat cgtattgggg aaccccgag atttgccag 1500
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<210> 47
<211> 48
<212> DNA
<213> Homo sapiens

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<400> 47
ccggcggaca tttatcacac agcagctgat gagaagtttc ttcattcca 48

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<210> 48
<211> 55
<212> DNA
<213> Artificial Sequence

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<220>
<221> misc_feature
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<400> 48
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<210> 49
<211> 49
<212> DNA
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<221> misc_feature
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<210> 50
<211> 1546
<212> DNA
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gggtggcggg caggacgccc gccataaact gccaggcatc aaattaagca gaaggccatc 240
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aaatatggac gtcgtactta acttttaag tatgggcaat caattgctcc tgttaaaatt 360
gcttttagaaa tacttttgga gcggtttgtt gtattgagtt tcatttgcg c attggttaaa 420
tggaagtga ccgtgcgctt actacagcct aatatttttg aaatatccca agagcttttt 480
ccttcgcatg cccacgctaa acattctttt tctcttttg ttaaactcgtt gtttgattta 540
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gattgacatt tgattctaataa aaattggatt tttgtcacac tattatatcg cttgaaatac 1200
aattgttttaa cataagtacc tgtaggatcg tacagggttta cgcaagaaaa tggtttggtta 1260
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<213> Artificial Sequence

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<210> 53
<211> 141
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<211> 147
<212> DNA
<213> Artificial Sequence

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<221> misc_feature
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tttttgtatg tctattggta gacgccacta tttaatagag accgccacaa ctgtatttat 120
ggtgaccgcc actatgactc gtgtagc 147

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<211> 55
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<211> 49
<212> DNA
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<223> Part of oligonucleotide duplex used in vector formation.

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<211> 668
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<211> 726
<212> DNA
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tcacgc 726

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<211> 44
<212> DNA
<213> Homo sapiens

<400> 59
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<210> 60
<211> 27
<212> DNA
<213> Homo sapiens

<400> 60
gtcctcctgg tacctaccta aaacaac 27

<210> 61
<211> 54
<212> DNA
<213> Homo sapiens

<400> 61
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<210> 62
<211> 19
<212> PRT
<213> Homo sapiens

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1 5 10 15

Gly Thr Tyr

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gtgtgataaa tgtccgccgg gtac 84

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<223> Sequence used in vector formation using human sequence with E. co
li codons

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ttggaggaaa agttttcca 78

<210> 65
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<212> DNA
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<220>
<221> misc_feature
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<400> 65

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<211> 38
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<400> 66
gtgctcctgg tacctaccta aaacagcact gcacagtg 38

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<210> 74
<211> 43
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<400> 74
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<210> 75
<211> 76
<212> DNA
<213> Mus musculus

<400> 75
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<210> 76
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<213> Mus musculus

<400> 76
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<210> 77
<211> 43
<212> DNA
<213> Homo sapiens

<400> 77
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<210> 78
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<212> DNA
<213> Homo sapiens

<400> 78
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<210> 79
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<212> DNA
<213> Mus musculus

<400> 79
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<210> 80
<211> 43
<212> DNA
<213> Mus musculus

<400> 80
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<210> 81
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<220>
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ccggaacag ataatgag 18

<210> 82
<211> 18
<212> DNA
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<220>
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<400> 82
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<210> 83
<211> 30
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<223> Part of oligonucleotide duplex used in vector formation.

<400> 83
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<210> 84
<211> 30
<212> DNA
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<210> 85
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
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<400> 85
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<210> 86
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
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<223> Part of oligonucleotide duplex used in vector formation.

<400> 86
gaccttcatt aaca 14

<210> 87
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
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 <223> Part of oligonucleotide duplex used in vector formation.

<400> 87
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<210> 88
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 <212> DNA
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<220>
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 <223> Part of oligonucleotide duplex used in vector formation.

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<210> 89
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
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 <223> Part of oligonucleotide duplex used in vector formation.

<400> 89
 tatgttccgg aaacagtgaa tcaactcaaa aataag 36

<210> 90
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
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 <223> Part of oligonucleotide duplex used in vector formation.

<400> 90
 gatccttatt tttgagttga ttcactgttt ccggaaca 38

<210> 91
 <211> 100
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <223> Part of oligonucleotide duplex used in vector formation.

<400> 91
 ctagcgacga cgacgacaaa gaaactctgc ctccaaaata cctgcattac gatccggaaa 60
 ctggtcatca gctgctgtgt cataaatgtg ctccgggtac 100

<210> 92
<211> 92
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Part of oligonucleotide duplex used in vector formation.

<400> 92
ccggagcaca tttatcacac agcagctgat gaccagtttc cggatcgtaa tgcaggtatt 60
ttggaggcag agtttctttg tcgtcgtcgt cg 92

<210> 93
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Used to produce fusion protein with human OPG.

<400> 93
acaaacacaa tcgatttgat actaga 26

<210> 94
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Used to produce fusion protein with human OPG.

<400> 94
tttgttttaa ctaattaaag gaggaataaa atatgagagg atcgcatcac 50

<210> 95
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Used to produce fusion protein with human OPG.

<400> 95
catcaccatc acgaaacctt cccgccgaaa tacctgcact acgacgaaga 50

<210> 96
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Used to produce fusion protein with human OPG.

<400> 96

aacctccac cagctgctgt gcgacaaatg cccgccgggt acccaaaca 49

<210> 97
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
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<223> Used to produce fusion protein with human OPG.

<400> 97
tgtttggtta cccggcgggc atttgt 26

<210> 98
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Used to produce fusion protein with human OPG.

<400> 98
cgcacagcag ctggtgggag gtttcttcgt cgtagtgcag gtatttcggc 50

<210> 99
<211> 49
<212> DNA
<213> Artificial Sequence

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<223> Used to produce fusion protein with human OPG.

<400> 99
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<210> 100
<211> 50
<212> DNA
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<220>
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<223> Used to produce fusion protein with human OPG.

<400> 100
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<210> 101
<211> 59
<212> DNA
<213> Homo sapiens

<400> 101
acaaacacaa tcgatttgat actagatttg tttaactaa ttaaaggagg aataaaatg 59

<210> 102
<211> 48
<212> DNA
<213> Homo sapiens

<400> 102
ctaattaaag gaggaataaa atgaaagaaa cttttcctcc aaaatatc 48

<210> 103
<211> 31
<212> DNA
<213> Homo sapiens

<400> 103
tgtttgggta cccggcggac atttatcaca c 31

<210> 104
<211> 59
<212> DNA
<213> Homo sapiens

<400> 104
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<210> 105
<211> 54
<212> DNA
<213> Homo sapiens

<400> 105
ctaattaaag gaggaataaa atgaaaaaaaa aagaaacttt tcctccaaaa tatc 54

<210> 106
<211> 31
<212> DNA
<213> Homo sapiens

<400> 106
tgtttgggta cccggcggac atttatcaca c 31

<210> 107
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for FchOPG fusion protein.

<400> 107
cagcccggtt aaaatggaaa cgtttcctcc aaaatatctt catt 44

<210> 108
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for FchOPG fusion protein.

<400> 108
cgtttccatt ttacccgggc tgagcgagag gctcttctgc gtgt 44

<210> 109
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for FcmuOPG fusion protein.

<400> 109
cgctcagccc gggtaaaatg gaaacgttgc ctccaaaata cctgc 45

<210> 110
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for FcmuOPG fusion protein.

<400> 110
ccattttacc cgggctgagc gagaggctct tctgcgtgt 39

<210> 111
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for muOPG-Fc fusion protein.

<400> 111
gaaaataaga tgcttagctg cagctgaacc aaaatc 36

<210> 112
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for muOPG-Fc fusion protein.

<400> 112
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<210> 113
<211> 36
<212> DNA

<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for huOPG-Fc fusion protein.

<400> 113
aaaaataagc tgcttagctg cagctgaacc aaaatc 36

<210> 114
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for huOPG-Fc fusion protein.

<400> 114
cagctgcagc taagcagctt atttttactg attgg 35

<210> 115
<211> 102
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Linker with XbaI and KpnI sites inserted into human sequence.

<400> 115
ctagaaggag gaataacata tggaaacttt tgctccaaaa tatcttcatt atgatgaaga 60
aactagtcac cagctgctgt gtgataaatg tccgccgggt ac 102

<210> 116
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Linker with XbaI and KpnI sites inserted into human sequence.

<400> 116
ccggcggaca tttatcacac agcagctgat gactagtttc ttcatacataa tgaagatatt 60
ttggagcaaa agtttccata tggtattcct cctt 94

<210> 117
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Linker with XbaI and SpeI sites inserted into human sequence.

<400> 117
ctagaaggag gaataacata tggaaacttt tcctgctaaa tatcttcatt atgatgaaga 60


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aa                                                                 62

<210> 118
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Linker with XbaI and SpeI sites inserted into human sequence.

<400> 118
ctagtttctt catcataatg aagatattta gcaggaaaag tttccatatg ttattcctcc 60
tt                                                                 62

<210> 119
<211> 51
<212> PRT
<213> Homo sapiens

<400> 119
Tyr His Tyr Tyr Asp Gln Asn Gly Arg Met Cys Glu Glu Cys His Met
1          5          10          15
Cys Gln Pro Gly His Phe Leu Val Lys His Cys Lys Gln Pro Lys Arg
20          25          30
Asp Thr Val Cys His Lys Pro Cys Glu Pro Gly Val Thr Tyr Thr Asp
35          40          45
Asp Trp His
50

<210> 120
<211> 2432
<212> DNA
<213> Rattus rattus

<220>
<221> CDS
<222> (124)..(1326)

<400> 120
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ggcagcagag aagcacctag cactggccca gcggctgccg cctgaggttt ccagaggacc 120
aca atg aac aag tgg ctg tgc tgt gca ctc ctg gtg ttc ttg gac atc 168
Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile
1          5          10          15
att gaa tgg aca acc cag gaa acc ttt cct cca aaa tac ttg cat tat 216
Ile Glu Trp Thr Thr Gln Glu Thr Phe Pro Lys Tyr Leu His Tyr
20          25          30
gac cca gaa acc gga cgt cag ctc ttg tgt gac aaa tgt gct cct ggc 264
Asp Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly
35          40          45

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acc	tac	cta	aaa	cag	cac	tgc	aca	gtc	agg	agg	aag	aca	ctg	tgt	gtc	312
Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	Val	Arg	Arg	Lys	Thr	Leu	Cys	Val	
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cct	tgc	cct	gac	tac	tct	tat	aca	gac	agc	tgg	cac	acg	agt	gat	gaa	360
Pro	Cys	Pro	Asp	Tyr	Ser	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	
	65					70					75					
tgc	gtg	tac	tgc	agc	ccc	gtg	tgc	aag	gaa	ctg	cag	acc	gtg	aaa	cag	408
Cys	Val	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Thr	Val	Lys	Gln	
80					85					90					95	
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Glu	Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Glu	Glu	Gly	Arg	
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tac	ctg	gag	ctc	gaa	ttc	tgc	ttg	aag	cac	cgg	agc	tgt	ccc	cca	ggc	504
Tyr	Leu	Glu	Leu	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	
			115					120					125			
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Leu	Gly	Val	Leu	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	
		130					135					140				
aga	tgt	ccg	gat	ggg	ttc	ttc	tca	ggg	gag	acg	tca	tcg	aaa	gca	ccc	600
Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	Gly	Glu	Thr	Ser	Ser	Lys	Ala	Pro	
	145					150					155					
tgt	agg	aaa	cac	acc	aac	tgc	agc	tca	ctt	ggc	ctc	ctg	cta	att	cag	648
Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	Ser	Leu	Gly	Leu	Leu	Leu	Ile	Gln	
160					165					170					175	
aaa	gga	aat	gca	aca	cat	gac	aat	gta	tgt	tcc	gga	aac	aga	gaa	gca	696
Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Val	Cys	Ser	Gly	Asn	Arg	Glu	Ala	
				180					185					190		
act	caa	aat	tgt	gaa	ata	gat	gtc	acc	ctg	tgc	gaa	gag	gca	ttc	ttc	744
Thr	Gln	Asn	Cys	Glu	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	
			195					200					205			
agg	ttt	gct	gtg	cct	acc	aag	att	ata	ccg	aat	tgg	ctg	agt	gtt	ctg	792
Arg	Phe	Ala	Val	Pro	Thr	Lys	Ile	Ile	Pro	Asn	Trp	Leu	Ser	Val	Leu	
		210					215					220				
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Val	Asp	Ser	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	
	225					230					235					
ata	aaa	cgg	aga	cac	agc	tcg	caa	gag	caa	act	ttc	cag	cta	ctt	aag	888
Ile	Lys	Arg	Arg	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	
240					245					250					255	
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Leu	Trp	Lys	His	Gln	Asn	Arg	Asp	Gln	Glu	Met	Val	Lys	Lys	Ile	Ile	
				260					265					270		
caa	gac	att	gac	ctc	tgt	gaa	agc	agt	gtg	caa	cgg	cat	atc	ggc	cac	984
Gln	Asp	Ile	Asp	Leu	Cys	Glu	Ser	Ser	Val	Gln	Arg	His	Ile	Gly	His	
			275					280					285			
gcg	aac	ctc	acc	aca	gag	cag	ctc	cgc	atc	ttg	atg	gag	agc	ttg	cct	1032
Ala	Asn	Leu	Thr	Thr	Glu	Gln	Leu	Arg	Ile	Leu	Met	Glu	Ser	Leu	Pro	
		290					295					300				

ggg aag aag atc agc cca gac gag att gag aga acg aga aag acc tgc Gly Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys 305 310 315	1080
aaa ccc agc gag cag ctc ctg aag cta ctg agc ttg tgg agg atc aaa Lys Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys 320 325 330 335	1128
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ttg aaa gca tac cac ttt ccc aaa acc gtc acc cac agt ctg agg aag Leu Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys 355 360 365	1224
acc atc agg ttc ttg cac agc ttc acc atg tac cga ttg tat cag aaa Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys 370 375 380	1272
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aagactatta cagtattgct atttatatcc atccag	2432

<210> 121
<211> 401
<212> PRT
<213> Rattus rattus

<400> 121

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile
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Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
50 55 60

Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
100 105 110

Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu
115 120 125

Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160

Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys
165 170 175

Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr
180 185 190

Gln Asn Cys Glu Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
195 200 205

Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val
210 215 220

Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
225 230 235 240

Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
245 250 255

Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln
260 265 270

Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His Ala
275 280 285

Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro Gly
290 295 300

Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys
305 310 315 320

Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu
340 345 350

Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr
355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu
370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
385 390 395 400

Leu

<210> 122
<211> 1325
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (91)..(1293)

<220>
<221> misc_feature
<223> At position 11, R is a purine.

<400> 122
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			Met	Asn	Lys	Trp	Leu	Cys	Cys	Ala						
			1				5									
ctc	ctg	gtg	ctc	ctg	gac	atc	att	gaa	tgg	aca	acc	cag	gaa	acc	ctt	162
Leu	Leu	Val	Leu	Leu	Asp	Ile	Ile	Glu	Trp	Thr	Thr	Gln	Glu	Thr	Leu	
	10					15					20					
ctt	cca	aag	tac	ttg	cat	tat	gac	cca	gaa	act	ggg	cat	cag	ctc	ctg	210
Leu	Pro	Lys	Tyr	Leu	His	Tyr	Asp	Pro	Glu	Thr	Gly	His	Gln	Leu	Leu	
25					30					35				40		
tgt	gac	aaa	tgt	gct	cct	ggc	acc	tac	cta	aaa	cag	cac	tgc	aca	gtg	258
Cys	Asp	Lys	Cys	Ala	Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	Val	
				45					50					55		
agg	agg	aag	aca	ttg	tgt	gtc	cct	tgc	cct	gac	cac	tct	tat	acg	gac	306
Arg	Arg	Lys	Thr	Leu	Cys	Val	Pro	Cys	Pro	Asp	His	Ser	Tyr	Thr	Asp	
			60					65					70			
agc	tgg	cac	acc	agt	gat	gag	tgt	gtg	tat	tgc	agc	cca	gtg	tgc	aag	354
Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	Val	Tyr	Cys	Ser	Pro	Val	Cys	Lys	
		75					80					85				
gaa	ctg	cag	tcc	gtg	aag	cag	gag	tgc	aac	cgc	acc	cac	aac	cga	gtg	402
Glu	Leu	Gln	Ser	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg	Val	
	90					95					100					
tgt	gag	tgt	gag	gaa	ggg	cgt	tac	ctg	gag	atc	gaa	ttc	tgc	ttg	aag	450
Cys	Glu	Cys	Glu	Glu		Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	
105					110					115					120	
cac	cgg	agc	tgt	ccc	ccg	ggc	tcc	ggc	gtg	gtg	caa	gct	gga	acc	cca	498
His	Arg	Ser	Cys	Pro	Pro	Gly	Ser	Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	
				125					130					135		
gag	cga	aac	aca	gtt	tgc	aaa	aaa	tgt	cca	gat	ggg	ttc	ttc	tca	ggt	546
Glu	Arg	Asn	Thr	Val	Cys	Lys	Lys	Cys	Pro	Asp	Gly	Phe	Phe	Ser	Gly	
			140					145					150			
gag	act	tca	tcg	aaa	gca	ccc	tgt	ata	aaa	cac	acg	aac	tgc	agc	aca	594
Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Ile	Lys	His	Thr	Asn	Cys	Ser	Thr	
		155				160						165				
ttt	ggc	ctc	ctg	cta	att	cag	aaa	gga	aat	gca	aca	cat	gac	aac	tgt	642
Phe	Gly	Leu	Leu	Leu	Ile	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Cys	
	170					175					180					
tgt	tcc	gga	aac	aga	gaa	gcc	acg	caa	aag	tgt	gga	ata	gat	gtc	acc	690
Cys	Ser	Gly	Asn	Arg	Glu	Ala	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	
185					190					195					200	
ctg	tgt	gaa	gag	gcc	ttc	ttc	agg	ttt	gct	gtt	cct	acc	aag	att	ata	738
Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	Lys	Ile	Ile	
				205					210					215		
cca	aat	tgg	ctg	agt	gtt	ttg	gtg	gac	agt	ttg	cct	ggg	acc	aaa	gtg	786
Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Ser	Leu	Pro	Gly	Thr	Lys	Val	
			220					225					230			
aat	gcc	gag	agt	gta	gag	agg	ata	aaa	cgg	aga	cac	agc	tca	caa	gag	834
Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Arg	His	Ser	Ser	Gln	Glu	
		235					240					245				

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<210> 123
<211> 401
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<223> At position 11, R is a purine.

<400> 123

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Leu Leu Asp Ile Ile
1          5          10          15

Glu Trp Thr Thr Gln Glu Thr Leu Leu Pro Lys Tyr Leu His Tyr Asp
          20          25          30

Pro Glu Thr Gly His Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
          35          40          45

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Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
50 55 60

Cys Pro Asp His Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Ser Val Lys Gln Glu
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser
115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys
130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160

Ile Lys His Thr Asn Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys
165 170 175

Gly Asn Ala Thr His Asp Asn Cys Cys Ser Gly Asn Arg Glu Ala Thr
180 185 190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
195 200 205

Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val
210 215 220

Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
225 230 235 240

Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
245 250 255

Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln
260 265 270

Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Leu Gly His Ser
275 280 285

Asn Leu Thr Thr Glu Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly
290 295 300

Lys Lys Ile Ser Pro Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys
305 310 315 320

Ser Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu
340 345 350

Lys Thr Ser His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr
355 360 365

Met Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu
370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
385 390 395 400

Leu

<210> 124
<211> 1356
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (95)..(1297)

<220>
<221> misc_feature
<223> At position 63, Y is a pyrimidine.

<400> 124
gtatatataa cgtgatgagc gtacgggtgc ggagacgcac cggcgcgctc gccagccgc 60

cgycaccaag cccctgaggt ttccggggac caca atg aac aag ttg ctg tgc tgc 115
Met Asn Lys Leu Leu Cys Cys
1 5

gcg ctc gtg ttt ctg gac atc tcc att aag tgg acc acc cag gaa acg 163
Ala Leu Val Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr
10 15 20

ttt cct cca aag tac ctt cat tat gac gaa gaa acc tct cat cag ctg 211
Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu
25 30 35

ttg tgt gac aaa tgt cct cct ggt acc tac cta aaa caa cac tgt aca 259
Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr
40 45 50 55

gca aag tgg aag tcc gtg tgc gcc cct tgc cct gac cac tac tac aca 307
Ala Lys Trp Lys Ser Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr

60						65						70						
gac	agc	tgg	cac	acc	agt	gac	gag	tgt	cta	tac	tgc	agc	ccc	gtg	tgc			355
Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	Pro	Val	Cys			
			75					80					85					
aag	gag	ctg	cag	tac	gtc	aag	cag	gag	tgc	aat	cgc	acc	cac	aac	cgc			403
Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg			
		90					95					100						
gtg	tgc	gaa	tgc	aag	gaa	ggg	cgc	tac	ctt	gag	ata	gag	ttc	tgc	ttg			451
Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu			
	105					110					115							
aaa	cat	agg	agc	tgc	cct	cct	gga	ttt	gga	gtg	gtg	caa	gct	gga	acc			499
Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr			
	120				125					130					135			
cca	gag	cga	aat	aca	gtt	tgc	aaa	aga	tgt	cca	gat	ggg	ttc	ttc	tca			547
Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser			
				140					145					150				
aat	gag	acg	tca	tct	aaa	gca	ccc	tgt	aga	aaa	cac	aca	aat	tgc	agt			595
Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	Cys	Ser			
			155					160					165					
gtc	ttt	ggt	ctc	ctg	cta	act	cag	aaa	gga	aat	gca	aca	cac	gac	aac			643
Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn			
		170					175					180						
ata	tgt	tcc	gga	aac	agt	gaa	tca	act	caa	aaa	tgt	gga	ata	gat	gtt			691
Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val			
	185					190					195							
acc	ctg	tgt	gag	gag	gca	ttc	ttc	agg	ttt	gct	gtt	cct	aca	aag	ttt			739
Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	Lys	Phe			
	200				205					210					215			
acg	cct	aac	tgg	ctt	agt	gtc	ttg	gta	gac	aat	ttg	cct	ggc	acc	aaa			787
Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Asn	Leu	Pro	Gly	Thr	Lys			
				220					225					230				
gta	aac	gca	gag	agt	gta	gag	agg	ata	aaa	cgg	caa	cac	agc	tca	caa			835
Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	Ser	Ser	Gln			
			235					240					245					
gaa	cag	act	ttc	cag	ctg	ctg	aag	tta	tgg	aaa	cat	caa	aac	aaa	gcc			883
Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	Lys	Ala			
		250					255					260						
caa	gat	ata	gtc	aag	aag	atc	atc	caa	gat	att	gac	ctc	tgt	gaa	aac			931
Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys	Glu	Asn			
	265					270					275							
agc	gtg	cag	cgg	cac	att	gga	cat	gct	aac	ctc	acc	ttc	gag	cag	ctt			979
Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala	Asn	Leu	Thr	Phe	Glu	Gln	Leu			
	280				285					290					295			
cgt	agc	ttg	atg	gaa	agc	tta	ccg	gga	aag	aaa	gtg	gga	gca	gaa	gac			1027
Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala	Glu	Asp			
				300					305					310				
att	gaa	aaa	aca	ata	aag	gca	tgc	aaa	ccc	agt	gac	cag	atc	ctg	aag			1075
Ile	Glu	Lys	Thr	Ile	Lys	Ala	Cys	Lys	Pro	Ser	Asp	Gln	Ile	Leu	Lys			

315										320										325										
ctg	ctc	agt	ttg	tgg	cga	ata	aaa	aat	ggc	gac	caa	gac	acc	ttg	aag		1123													
Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys															
		330					335					340																		
ggc	cta	atg	cac	gca	cta	aag	cac	tca	aag	acg	tac	cac	ttt	ccc	aaa		1171													
Gly	Leu	Met	His	Ala	Leu	Lys	His	Ser	Lys	Thr	Tyr	His	Phe	Pro	Lys															
	345					350					355																			
act	gtc	act	cag	agt	cta	aag	aag	acc	atc	agg	ttc	ctt	cac	agc	ttc		1219													
Thr	Val	Thr	Gln	Ser	Leu	Lys	Lys	Thr	Ile	Arg	Phe	Leu	His	Ser	Phe															
360					365					370					375															
aca	atg	tac	aaa	ttg	tat	cag	aag	tta	ttt	tta	gaa	atg	ata	ggt	aac		1267													
Thr	Met	Tyr	Lys	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	Gly	Asn															
			380						385					390																
cag	gtc	caa	tca	gta	aaa	ata	agc	tgc	tta	taactggaaa	tggccattga						1317													
Gln	Val	Gln	Ser	Val	Lys	Ile	Ser	Cys	Leu																					
		395						400																						
gctgtttcct cacaattggc gagatcccat ggatgataa																1356														
<210> 125																														
<211> 401																														
<212> PRT																														
<213> Homo sapiens																														
<220>																														
<221> misc_feature																														
<223> At position 63, Y is a pyrimidine.																														
<400> 125																														
Met	Asn	Lys	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile															
1				5					10					15																
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp															
			20					25					30																	
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr															
		35				40						45																		
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Ser	Val	Cys	Ala	Pro															
	50					55					60																			
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys															
65					70					75					80															
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu															
			85						90					95																
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr															
			100					105					110																	

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
130 135 140

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
165 170 175

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
180 185 190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
195 200 205

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
210 215 220

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
225 230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
245 250 255

Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln
260 265 270

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala
275 280 285

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
290 295 300

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
305 310 315 320

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
340 345 350

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr
355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu
370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
385 390 395 400

Leu

<210> 126
<211> 139
<212> PRT
<213> Homo sapiens

<400> 126

Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys
1 5 10 15

Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
20 25 30

Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala
35 40 45

Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys
50 55 60

Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr
65 70 75 80

Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn
85 90 95

Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His
100 105 110

Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly
115 120 125

Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys
130 135

<210> 127
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Oligonucleotide capable of hybridizing to human sequence.

<400> 127
acctacttct ttgaagagta gtcgacgaca cactatttac aggcggcc

48

<210> 128
<211> 219
<212> PRT
<213> Rattus rattus

<400> 128

Met	Leu	Gly	Ile	Trp	Thr	Leu	Leu	Pro	Leu	Val	Leu	Thr	Ser	Val	Ala	
1				5					10					15		
Arg	Leu	Ser	Ser	Lys	Ser	Val	Asn	Ala	Gln	Val	Thr	Asp	Ile	Asn	Ser	
			20					25					30			
Lys	Gly	Leu	Glu	Leu	Arg	Lys	Thr	Val	Thr	Thr	Val	Glu	Thr	Gln	Asn	
		35					40					45				
Leu	Glu	Gly	Leu	His	His	Asp	Gly	Gln	Phe	Cys	His	Lys	Pro	Cys	Pro	
	50					55					60					
Pro	Gly	Glu	Arg	Lys	Ala	Arg	Asp	Cys	Thr	Val	Asn	Gly	Asp	Glu	Pro	
65					70					75					80	
Asp	Cys	Val	Pro	Cys	Gln	Glu	Gly	Lys	Glu	Tyr	Thr	Asp	Lys	Ala	His	
				85					90					95		
Phe	Ser	Ser	Lys	Cys	Arg	Arg	Cys	Arg	Leu	Cys	Asp	Glu	Gly	His	Gly	
			100					105					110			
Leu	Glu	Val	Glu	Ile	Asn	Cys	Thr	Arg	Thr	Gln	Asn	Thr	Lys	Cys	Arg	
		115					120					125				
Cys	Lys	Pro	Asn	Phe	Phe	Cys	Asn	Ser	Thr	Val	Cys	Glu	His	Cys	Asp	
	130					135					140					
Pro	Cys	Thr	Lys	Cys	Glu	His	Gly	Ile	Ile	Lys	Glu	Cys	Thr	Leu	Thr	
145					150					155					160	
Ser	Asn	Thr	Lys	Cys	Lys	Glu	Glu	Gly	Ser	Arg	Ser	Asn	Leu	Gly	Trp	
				165					170					175		
Leu	Cys	Leu	Leu	Leu	Leu	Pro	Ile	Pro	Leu	Ile	Val	Trp	Val	Lys	Arg	
			180					185					190			
Lys	Glu	Val	Gln	Lys	Thr	Cys	Arg	Lys	His	Arg	Lys	Glu	Asn	Gln	Gly	
		195					200					205				
Ser	His	Glu	Ser	Pro	Thr	Leu	Asn	Pro	Glu	Thr						
	210					215										

<210> 129

<211> 281

<212> PRT

<213> Rattus rattus

<400> 129

Met	Gly	Leu	Ser	Thr	Val	Pro	Asp	Leu	Leu	Leu	Pro	Leu	Val	Leu	Leu	
1				5					10					15		
Glu	Leu	Leu	Val	Gly	Ile	Tyr	Pro	Ser	Gly	Val	Ile	Gly	Leu	Val	Pro	
			20					25					30			
His	Leu	Gly	Asp	Arg	Glu	Lys	Arg	Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys	
		35					40					45				
Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile	Cys	Cys	Thr	Lys	Cys	His	Lys	
	50					55					60					
Gly	Thr	Tyr	Leu	Thr	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	

65					70					75					80
Asp	Cys	Arg	Glu	Cys 85	Glu	Ser	Gly	Ser	Phe 90	Thr	Ala	Ser	Glu	Asn 95	His
Leu	Arg	His	Cys 100	Leu	Ser	Cys	Ser	Lys 105	Cys	Arg	Lys	Glu	Met 110	Gly	Gln
Val	Glu	Ile 115	Ser	Ser	Cys	Thr	Val 120	Asp	Arg	Asp	Thr	Val 125	Cys	Gly	Cys
Arg	Lys 130	Asn	Gln	Tyr	Arg	His 135	Tyr	Trp	Ser	Glu	Asn 140	Leu	Phe	Gln	Cys
Phe	Asn 145	Cys	Ser	Leu	Cys 150	Leu	Asn	Gly	Thr	Val 155	His	Leu	Ser	Cys	Gln
Glu	Lys	Gln	Asn	Thr 165	Val	Cys	Thr	Cys	His 170	Ala	Gly	Phe	Phe	Leu	Arg
Glu	Asn	Glu	Cys 180	Val	Ser	Cys	Ser	Asn 185	Cys	Lys	Lys	Ser	Leu	Glu	Cys
Thr	Lys 195	Leu	Cys	Leu	Pro	Gln	Ile 200	Glu	Asn	Val	Lys	Gly 205	Thr	Glu	Asp
Ser	Gly 210	Thr	Thr	Val	Leu	Leu 215	Pro	Leu	Val	Ile	Phe 220	Phe	Gly	Leu	Cys
Leu	Leu	Ser	Leu	Leu	Phe 230	Ile	Gly	Leu	Met	Thr 235	Arg	Thr	Gln	Arg	Trp 240
Lys	Ser	Lys	Leu	Tyr 245	Ser	Ile	Val	Cys	Gly 250	Lys	Ser	Thr	Pro	Glu 255	Lys
Glu	Gly	Glu	Leu 260	Glu	Gly	Thr	Thr	Thr 265	Lys	Pro	Leu	Ala	Pro 270	Asn	Pro
Ser	Phe 275	Ser	Pro	Thr	Pro	Gly	Phe 280	Thr							

<210> 130
 <211> 207
 <212> PRT
 <213> Rattus rattus

<400> 130

Met	Leu	Arg	Leu	Ile	Ala	Leu	Leu	Val	Cys	Val	Val	Tyr	Val	Tyr	Gly
1				5					10					15	
Asp	Asp	Val	Pro	Tyr	Ser	Ser	Asn	Gln	Gly	Lys	Cys	Gly	Gly	His	Asp
			20					25					30		
Tyr	Glu	Lys	Asp	Gly	Leu	Cys	Cys	Ala	Ser	Cys	His	Pro	Gly	Phe	Tyr
		35					40					45			
Ala	Ser	Arg	Leu	Cys	Gly	Pro	Gly	Ser	Asn	Thr	Val	Cys	Ser	Pro	Cys
		50				55					60				
Glu	Asp	Gly	Thr	Phe	Thr	Ala	Ser	Thr	Asn	His	Ala	Pro	Ala	Cys	Val
65					70					75				80	
Ser	Cys	Arg	Gly	Pro	Cys	Thr	Gly	His	Leu	Ser	Glu	Ser	Gln	Pro	Cys

				85				90				95			
Asp	Arg	Thr	His 100	Asp	Arg	Val	Cys	Asn 105	Cys	Ser	Thr	Gly	Asn 110	Tyr	Cys
Leu	Leu	Lys 115	Gly	Gln	Asn	Gly	Cys 120	Arg	Ile	Cys	Ala	Pro 125	Gln	Thr	Lys
Cys	Pro 130	Ala	Gly	Tyr	Gly	Val 135	Ser	Gly	His	Thr	Arg 140	Ala	Gly	Asp	Thr
Leu 145	Cys	Glu	Lys	Cys	Pro 150	Pro	His	Thr	Tyr	Ser 155	Asp	Ser	Leu	Ser	Pro 160
Thr	Glu	Arg	Cys	Gly 165	Thr	Ser	Phe	Asn	Tyr 170	Ile	Ser	Val	Gly	Phe 175	Asn
Leu	Tyr	Pro	Val 180	Asn	Glu	Thr	Ser	Cys 185	Thr	Thr	Thr	Ala	Gly 190	His	Asn
Glu	Val	Ile 195	Lys	Thr	Lys	Glu	Phe 200	Thr	Val	Thr	Leu	Asn 205	Tyr	Thr	
<210>		131													
<211>		227													
<212>		PRT													
<213>		Rattus rattus													
<400>		131													
Met 1	Ala	Pro	Val	Ala 5	Val	Trp	Ala	Ala	Leu 10	Ala	Val	Gly	Leu	Glu 15	Leu
Trp	Ala	Ala	Ala 20	His	Ala	Leu	Pro	Ala 25	Gln	Val	Ala	Phe	Thr 30	Pro	Tyr
Ala	Pro	Glu 35	Pro	Gly	Ser	Thr	Cys 40	Arg	Leu	Arg	Glu	Thr 45	Thr	Asp	Gln
Thr	Ala	Gln	Met	Cys	Cys	Ser 55	Lys	Cys	Ser	Pro	Gly 60	Gln	His	Ala	Lys
Val 65	Phe	Cys	Thr	Lys	Thr 70	Ser	Asp	Thr	Val	Cys 75	Asp	Ser	Cys	Glu	Asp 80
Ser	Thr	Tyr	Thr	Gln 85	Leu	Trp	Asn	Trp	Val 90	Pro	Glu	Cys	Leu	Ser 95	Cys
Gly	Ser	Arg	Cys 100	Ser	Ser	Asp	Gln	Val 105	Glu	Thr	Gln	Ala	Cys 110	Thr	Arg
Glu	Gln	Asn 115	Arg	Ile	Cys	Thr	Cys 120	Arg	Pro	Gly	Trp	Tyr 125	Cys	Ala	Leu
Ser	Lys 130	Gln	Glu	Gly	Cys	Arg 135	Leu	Cys	Ala	Pro	Leu 140	Arg	Lys	Cys	Arg
Pro 145	Gly	Phe	Gly	Val	Ala 150	Arg	Pro	Gly	Thr	Glu 155	Thr	Ser	Asp	Val	Val 160
Cys	Lys	Pro	Cys	Ala 165	Pro	Gly	Thr	Phe	Ser 170	Asn	Thr	Thr	Ser	Ser 175	Thr
Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly

	180		185		190
Asn	Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser				
	195		200		205
Met	Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser				
	210		215		220
Gln	His Thr				
	225				
<210>	132				
<211>	197				
<212>	PRT				
<213>	Rattus rattus				
<400>	132				
Met	Val Ser Leu Pro Arg Leu Cys Ala Leu Trp Gly Cys Leu Leu Thr				
	1	5		10	15
Ala	Val His Leu Gly Gln Cys Val Thr Cys Ser Asp Lys Gln Tyr Leu				
	20		25		30
His	Asp Gly Gln Cys Cys Asp Leu Cys Gln Pro Gly Ser Arg Leu Thr				
	35		40		45
Ser	His Cys Thr Ala Leu Glu Lys Thr Gln Cys His Pro Cys Asp Ser				
	50		55		60
Gly	Glu Phe Ser Ala Gln Trp Asn Arg Glu Ile Arg Cys His Gln His				
	65	70		75	80
Arg	His Cys Glu Pro Asn Gln Gly Leu Arg Val Lys Lys Glu Gly Thr				
	85		90		95
Ala	Glu Ser Asp Thr Val Cys Thr Cys Lys Glu Gly Gln His Cys Thr				
	100		105		110
Ser	Lys Asp Cys Glu Ala Cys Ala Gln His Thr Pro Cys Ile Pro Gly				
	115		120		125
Phe	Gly Val Met Glu Met Ala Thr Glu Thr Thr Asp Thr Val Cys His				
	130		135		140
Pro	Cys Pro Val Gly Phe Phe Ser Asn Gln Ser Ser Leu Phe Glu Lys				
	145	150		155	160
Cys	Tyr Pro Trp Thr Ser Cys Glu Asp Lys Asn Leu Glu Val Leu Gln				
	165		170		175
Lys	Gly Thr Ser Gln Thr Asn Val Ile Cys Gly Leu Lys Ser Arg Met				
	180		185		190
Arg	Ala Leu Leu Val				
	195				
<210>	133				
<211>	208				
<212>	PRT				
<213>	Rattus rattus				
<400>	133				

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile
1 5 10 15
Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
20 25 30
Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
35 40 45
Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
50 55 60
Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80
Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu
85 90 95
Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
100 105 110
Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu
115 120 125
Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
130 135 140
Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160
Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys
165 170 175
Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr
180 185 190
Gln Asn Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
195 200 205
<210> 134
<211> 224
<212> PRT
<213> Rattus rattus
<400> 134

Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu
1 5 10 15
Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys
20 25 30
Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn
35 40 45
Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys
50 55 60
Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
65 70 75 80
Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
85 90 95

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
100 105 110
Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
115 120 125
Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
130 135 140
Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
145 150 155 160
Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
165 170 175
Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
180 185 190
Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
195 200 205
Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile
210 215 220

<210> 135
<211> 205
<212> PRT
<213> Rattus rattus

<400> 135

Met Tyr Val Trp Val Gln Gln Pro Thr Ala Phe Leu Leu Leu Gly Leu
1 5 10 15
Ser Leu Gly Val Thr Val Lys Leu Asn Cys Val Lys Asp Thr Tyr Pro
20 25 30
Ser Gly His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val
35 40 45
Ser Arg Cys Asp His Thr Arg Asp Thr Val Cys His Pro Cys Glu Pro
50 55 60
Gly Phe Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr
65 70 75 80
Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr Pro
85 90 95
Thr Glu Asp Thr Val Cys Gln Cys Arg Pro Gly Thr Gln Pro Arg Gln
100 105 110
Asp Ser Ser His Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly
115 120 125
His Phe Ser Pro Gly Ser Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys
130 135 140
Thr Leu Ser Gly Lys Gln Ile Arg His Pro Ala Ser Asn Ser Leu Asp
145 150 155 160
Thr Val Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr
165 170 175

Gln Arg Thr Thr Phe Arg Pro Thr Thr Val Pro Ser Thr Thr Val Trp
180 185 190

Pro Arg Thr Ser Gln Leu Pro Ser Thr Pro Thr Leu Val
195 200 205

<210> 136
<211> 191
<212> PRT
<213> Rattus rattus

<400> 136

Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val
1 5 10 15

Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln
20 25 30

Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
35 40 45

Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys
50 55 60

Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
65 70 75 80

His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
85 90 95

Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr
100 105 110

Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn
115 120 125

Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg
130 135 140

Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro
145 150 155 160

Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu
165 170 175

Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu
180 185 190

<210> 137
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Oligonucleotide capable of hybridizing to human sequence.

<400> 137
tatggatgaa gaaacttctc atcagctgct gtgtgataaa tgtccgccgg gtac

54

<210> 138
<211> 284

<212> PRT
<213> Mus musculus

<400> 138

Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Ser	Gly	Val	Val	Gln	Ala	
1				5					10					15		
Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Lys	Cys	Pro	Asp	Gly	Phe	
			20					25					30			
Phe	Ser	Gly	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Ile	Lys	His	Thr	Asn	
		35					40					45				
Cys	Ser	Thr	Phe	Gly	Leu	Leu	Leu	Ile	Gln	Lys	Gly	Asn	Ala	Thr	His	
	50					55					60					
Asp	Asn	Val	Cys	Ser	Gly	Asn	Arg	Glu	Ala	Thr	Gln	Lys	Cys	Gly	Ile	
65					70					75					80	
Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	
				85					90					95		
Lys	Ile	Ile	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Ser	Leu	Pro	Gly	
			100					105					110			
Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Arg	His	Ser	
		115					120					125				
Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	
	130					135					140					
Arg	Asp	Gln	Glu	Met	Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Ala	Leu	Cys	
145					150					155					160	
Glu	Ser	Ser	Val	Gln	Arg	His	Leu	Gly	His	Ser	Asn	Leu	Thr	Thr	Glu	
				165					170					175		
Gln	Leu	Leu	Ala	Leu	Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Ile	Ser	Pro	
			180					185					190			
Glu	Glu	Ile	Glu	Arg	Thr	Arg	Lys	Thr	Cys	Lys	Ser	Ser	Glu	Gln	Leu	
		195					200					205				
Leu	Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	
	210					215					220					
Leu	Lys	Gly	Leu	Met	Tyr	Ala	Leu	Lys	His	Leu	Lys	Thr	Ser	His	Phe	
225					230					235					240	
Pro	Lys	Thr	Val	Thr	His	Ser	Leu	Arg	Lys	Thr	Met	Arg	Phe	Leu	His	
				245					250					255		
Ser	Phe	Thr	Met	Tyr	Arg	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	
			260					265					270			
Gly	Asn	Gln	Val	Gln	Ser	Val	Lys	Ile	Ser	Cys	Leu					
		275					280									

<210> 139
<211> 380
<212> PRT
<213> Homo sapiens

<400> 139

Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	Glu	Glu	Thr	Ser	His
1				5					10					15	
Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His
			20					25					30		
Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	Cys	Pro	Asp	His	Tyr
		35					40					45			
Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	Pro
	50					55					60				
Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His
65					70					75					80
Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe
				85					90					95	
Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala
			100					105					110		
Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe
		115					120					125			
Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn
	130					135					140				
Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His
145					150					155					160
Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile
				165					170					175	
Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr
			180					185					190		
Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Asn	Leu	Pro	Gly
		195					200					205			
Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	Ser
	210					215					220				
Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn
225					230					235					240
Lys	Ala	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys
				245					250					255	
Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala	Asn	Leu	Thr	Phe	Glu
			260					265					270		
Gln	Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala
		275					280					285			
Glu	Asp	Ile	Glu	Lys	Thr	Ile	Lys	Ala	Cys	Lys	Pro	Ser	Asp	Gln	Ile
	290					295					300				
Leu	Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr
305					310					315					320
Leu	Lys	Gly	Leu	Met	His	Ala	Leu	Lys	His	Ser	Lys	Thr	Lys	His	Phe
				325					330					335	

Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His
340 345 350

Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile
355 360 365

Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
370 375 380

<210> 140
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for deletion analogue.

<400> 140
tggaccaccc agaagtacct tcattatgac 30

<210> 141
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for deletion analogue.

<400> 141
gtcataatga aggtacttct ggtggtcca 30

<210> 142
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for deletion analogue.

<400> 142
ggaccacca gcttcattat gacgaagaaa c 31

<210> 143
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for deletion analogue.

<400> 143
gtttcttcgt cataatgaag ctgggtgggc c 31

<210> 144
<211> 29

<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for deletion analogue.

<400> 144
gtggaccacc caggacgaag aaacctctc 29

<210> 145
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for deletion analogue.

<400> 145
gagaggtttc ttcgtcctgg gtggtccac 29

<210> 146
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for mutant analogue.

<400> 146
cgtttctctcc aaagttcctt cattatgac 29

<210> 147
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for mutant analogue.

<400> 147
gtcataatga aggaactttg gaggaaacg 29

<210> 148
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for mutant analogue.

<400> 148
ggaaacggtt cctgcaaagt accttcatta tg 32

<210> 149
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for mutant analogue.

<400> 149
cataatgaag gtactttgca ggaaacgttt cc 32

<210> 150
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for mutant analogue.

<400> 150
cacgcaaaag tcgggaatag atgtcac 27

<210> 151
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for mutant analogue.

<400> 151
gtgacatcta ttcccgactt ttgcgtg 27

<210> 152
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for mutant analogue.

<400> 152
cacctgtcg gaagaggcct tcttc 25

<210> 153
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for mutant analogue.

<400> 153
gaagaaggcc tcttccgaca gggtg 25

<210> 154
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for mutant analogue.

<400> 154
tgacctctcg gaaagcagcg tgca 24

<210> 155
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for mutant analogue.

<400> 155
tgcacgctgc tttccgagag gtca 24

<210> 156
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for mutant analogue.

<400> 156
cctcgaaatc gagcgagcag ctcc 24

<210> 157
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for mutant analogue.

<400> 157
cgatttcgag gtctttctcg ttctc 25

<210> 158
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for mutant analogue.

<400> 158
ccgtgaaaat aagctcgta taactaggaa tgg 33

<210> 159
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for mutant analogue.

<400> 159
ccatttcctag ttataacgag cttattttca cgg 33

<210> 160
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for deletion mutant.

<400> 160
cctctgagct caagcttccg aggaccacaa tgaacaag 38

<210> 161
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for deletion mutant.

<400> 161
cctctctcga gtcagggtgac atctattcca cactttttgcg tggc 44

<210> 162
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for deletion mutant.

<400> 162
cctctgagct caagcttccg aggaccacaa tgaacaag 38

<210> 163
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for deletion mutant.

<400> 163
cctctctcga gtcaaggaac agcaaacctg aagaaggc 38

<210> 164
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for deletion mutant.

<400> 164
cctctgagct caagcttccg aggaccacaa tgaacaag 38

<210> 165
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for deletion mutant.

<400> 165
cctctctcga gtcactctgt ggtgagggtc gagtggcc 38

<210> 166
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for deletion mutant.

<400> 166
cctctgagct caagcttccg aggaccacaa tgaacaag 38

<210> 167
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for deletion mutant.

<400> 167
cctctctcga gtcaggatgt tttcaagtgc ttgagggc 38

<210> 168
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Encoded by oligonucleotide duplex used in vector formation.

C1F7
Sub B,
a.

<400> 168

Concluded

Met Lys His His His His His His His Ala Ser Val Asn Ala Leu Glu
1 5 10 15
